Genetic Diversity and Relationship among 19 Accessions of Sorghum-Sudangrass Hybrids as Revealed by SSR Markers

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Genetic diversity and relationship among 19 accessions of Sorghum-sudangrass hybrids as revealed by SSR markers

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Introduction

Sorghum (*Sorghum bicolor*) and sudangrass (*S. sudanense*) are two members of the agriculturally important genus *Sorghum*. Hybrids of these two species have exhibited favorable forage yields and overall improved quality and disease resistance (Zhan and Qian, 2004). Sorghum–sudangrass hybrids (*Sorghum bicolor* × *S. sudanense*) are used as a forage crop and recommended as an alternative to corn in USA (Kilcer *et al*., 2003). In recent years, the planting areas of sorghum–sudangrass hybrids have increased in China. SSR has been widely employed in crop germplasm identification, genetic mapping and diversity analysis (Zhan *et al*., 2008, Li *et al*., 2010). However, no reports have been published on studies of the genetic diversity of main sorghum–sudangrass hybrids in China. The objective of this current study was to evaluate the genetic diversity and relationship among 19 accessions of sorghum-sudangrass hybrids as revealed by SSR markers.

Materials and Methods

19 accessions of sorghum-sudangrass hybrids and one accession from each of three related species (*S. sorghum*, *S. Sudanense*, and *Zea mays*) were included in the study (Table 1). DNA extraction and SSR PCR reactions were performed as described (Zhan *et al*., 2008). A molecular marker data matrix was established by recording 1 for the presence of a specific band and 0 for the absence of the band. Statistical analysis software, NTSYS-pc, was used, in which the measure of similarity coefficient was Dice (Rohlf, 2000). The UPGMA method was used for cluster analysis and phylogenetic tree construction. Gene diversity was evaluated with the polymorphic information content (PIC) (Zhan *et al*., 2008).

Table 1: The name, type and source of 22 accessions tested

NO.	Name	Type	Source
1	Everlush	*S. bicolor* × *S. sudanense*	Australia
2	MMR327/36	*S. bicolor* × *S. sudanense*	USA
3	MMR327/38	*S. bicolor* × *S. sudanense*	USA
4	Verdeo-45	*S. bicolor* × *S. sudanense*	Argentina
5	MMR352/40	*S. bicolor* × *S. sudanense*	USA
6	Pacesetter	*S. bicolor* × *S. sudanense*	USA
7	Sweet N Honey II	*S. bicolor* × *S. sudanense*	USA
8	Evergreen	*S. bicolor* × *S. sudanense*	USA
9	Pioneer	*S. bicolor* × *S. sudanense*	USA
10	Wancao No.3	*S. bicolor* × *S. sudanense*	Anhui,China
11	Jincao No.5	*S. bicolor* × *S. sudanense*	Shanxi,China
12	Jincao No.1	*S. bicolor* × *S. sudanense*	Shanxi,China
13	Jicao No.2	*S. bicolor* × *S. sudanense*	Hebei,China
14	S.Africa-Su	*S. bicolor* × *S. sudanense*	South Africa
15	Wancao No.2	*S. bicolor* × *S. sudanense*	Anhui,China
16	Jincao No.6	*S. bicolor* × *S. sudanense*	Shanxi,China
17	Jicao No.1	*S. bicolor* × *S. sudanense*	Hebei,China
18	Jicao No.3	*S. bicolor* × *S. sudanense*	Hebei,China
19	BMR1	*S. bicolor* × *S. sudanense*	Shanxi,China
20	TX623A	*S. sorghum*	USA
21	S722	*S. sudanense*	India
22	Yunyou 199	*Z. mays*	Yunnan,China

Results and Discussion

The 79 SSR primer pairs generated a total of 259 polymorphic alleles, with an average of 3.28 alleles per locus, and a range of 1 to 7 alleles. The polymorphic rate was 91.89% within 22 accessions, and the average genetic diversity (PIC) value was 0.440. Except three relatives (sorghum, sudangrass and maize), a total of 222 polymorphic alleles were generated within 19 sorghum-sudangrass hybrids, with a polymorphism rate of 79.73%. The SSR profile generated by primer *astu*224 was shown in Figure 1. The PIC value was 0.421. Genetic similarity (GS) values between all varieties ranged from 0.376 to 0.923 and were used to produce a dendrogram (Figure 2). The 22 accessions were clustered into three groups (GS=0.696), specifically, group I (sorghum-sudangrass hybrids), group II (sorghum and sudangrass), group III (maize). Results of our analyses suggest the sudangrass/sorghum relationship is sufficiently close, but the hybrids reveal obvious heterosis. Therefore, all accessions of sorghum-sudangrass hybrids were clustered into one group. GS values between 19 sorghum-sudangrass hybrids ranged from 0.646 to 0.923.

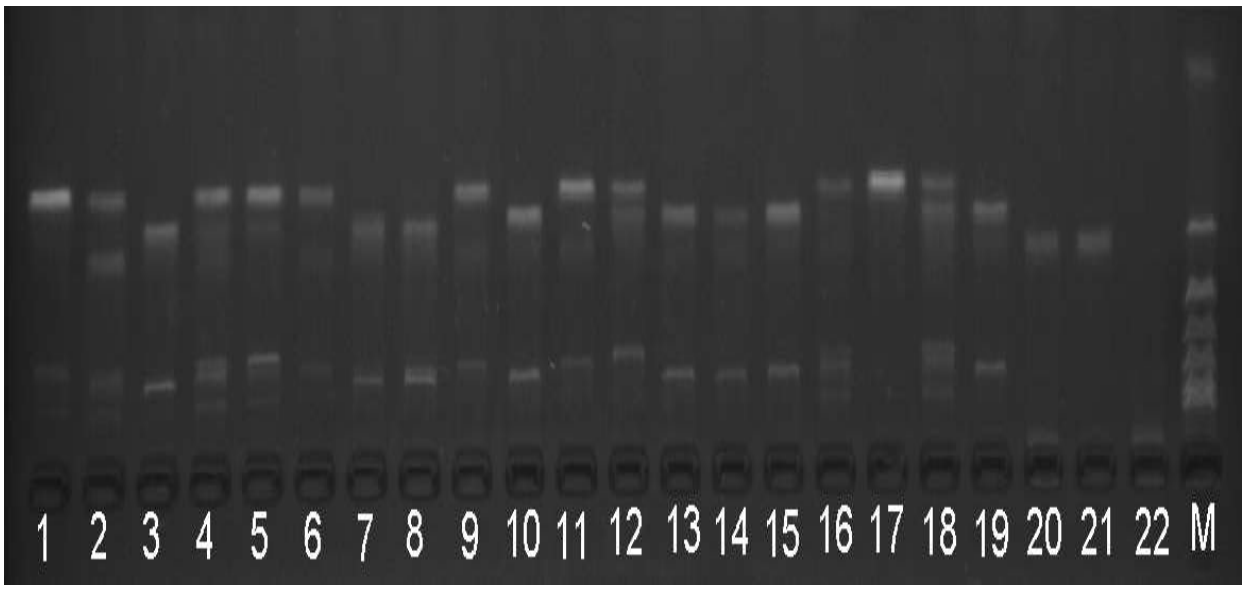

Fig 1: The amplification results of primer ***astu***224 in the 22 cultivars

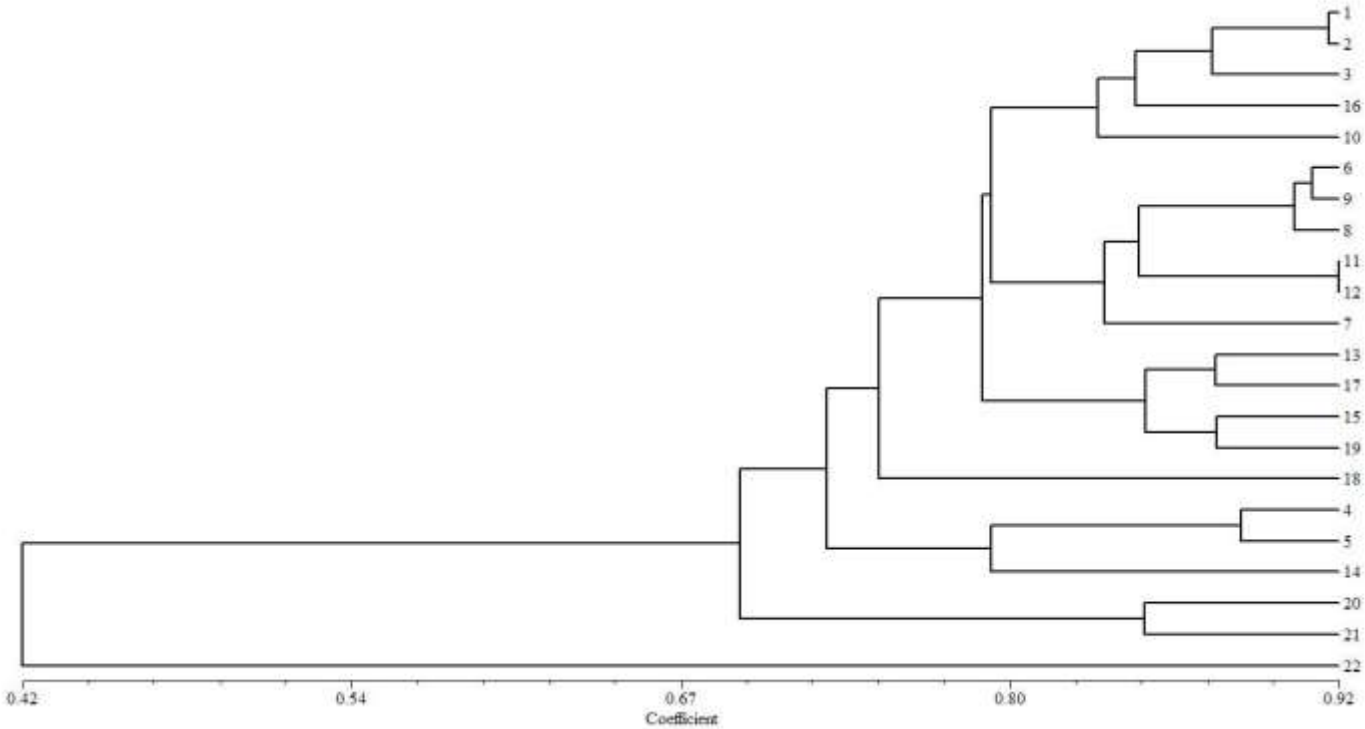

Fig 2: The clustering result of 22 cultivars based on SSR coefficient

Conclusion

Except three relatives (sorghum, sudangrass and maize), a total of 222 polymorphic alleles were generated within 19 sorghum-sudangrass hybrids, with a polymorphism rate of 79.73%. The PIC value was 0.421. These varieties from the same region, especially those from the same breeding institution, exhibited small genetic variations and high genetic similarities. At present, more attention should be paid to discovery and innovation in the breeding of sorghum-sudangrass hybrids.

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